



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 1835977

TO: Sheela Huff
Location: 3a15 / 3c18
Monday, April 03, 2006
Art Unit: 1643
Phone: 571-272-0834
Serial Number: 10 / 645761

From: Jan Delaval
Location: Biotech-Chem Library
Remsen 1a51
Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes

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71973
STIC-Biotech/ChemLib

183597

mg

From: Huff, Sheela
Sent: Thursday, March 30, 2006 6:24 AM
To: STIC-Biotech/ChemLib
Subject: search for 10/645761

please search and interference SEQ ID NO. 2 of the above.

thans-

Sheela Huff
Art Unit 1643
571-272-0834
Remsen 3A15
mailbox Remsen 3C18

RECEIVED
MAR 30 2006
STIC-BIOTECH

Searcher: an
Searcher Phone: 722504
Date Searcher Picked up: 4/3/06
Date completed: 4/3/06
Searcher Prep Time: 10
Online Time: 22

Type of Search
NA# _____ AA# ✓
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: ✓
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:26:33 ; Search time 38 Seconds
(without alignments)
577.301 Million cell updates/sec

Title: US-10-645-761-2
Perfect score: 1238
Sequence: 1 MDKTHCPPCPAPELGPGS.....MHEALHNHYTKSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1233 | 99.6 | 255 | 4 | S31866 |
| 2 | 1233 | 99.6 | 330 | 1 | GHU |
| 3 | 1227 | 99.1 | 374 | 2 | S69339 |
| 4 | 1180 | 95.3 | 234 | 2 | PT0207 |
| 5 | 1146 | 92.6 | 377 | 2 | A23511 |
| 6 | 1144 | 92.4 | 377 | 2 | A60764 |
| 7 | 1142.5 | 92.3 | 326 | 1 | G2HU |
| 8 | 1135 | 91.7 | 327 | 1 | G4HU |
| 9 | 1121 | 90.5 | 289 | 1 | G3HUMI |
| 10 | 918.5 | 74.2 | 323 | 1 | GHRB |
| 11 | 906.5 | 73.2 | 328 | 2 | I47160 |
| 12 | 906.5 | 73.2 | 328 | 2 | I47159 |
| 13 | 903.5 | 73.0 | 277 | 2 | I47162 |
| 14 | 889 | 71.8 | 329 | 1 | G2GP |
| 15 | 895.5 | 71.5 | 328 | 2 | I47158 |
| 16 | 878.5 | 71.0 | 328 | 2 | I47161 |
| 17 | 855.5 | 69.1 | 470 | 2 | S22080 |
| 18 | 846 | 68.3 | 308 | 2 | C30554 |
| 19 | 831.5 | 68.3 | 472 | 2 | S31459 |
| 20 | 845.5 | 68.3 | 329 | 1 | G3MSC |
| 21 | 838 | 67.7 | 333 | 2 | PS0018 |
| 22 | 834.5 | 67.4 | 398 | 1 | G3MSM |
| 23 | 827.5 | 66.8 | 444 | 2 | FC4436 |
| 24 | 818.5 | 66.1 | 326 | 2 | PS0017 |
| 25 | 817.5 | 66.0 | 324 | 1 | G1MS |
| 26 | 812.5 | 65.6 | 393 | 1 | G1MSM |
| 27 | 809.5 | 65.4 | 329 | 2 | S00847 |
| 28 | 809 | 65.3 | 330 | 1 | G2MSA |
| 29 | 809 | 65.3 | 469 | 2 | S37483 |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 804 | 64.9 | 399 | 1 | G2MSAM | Ig gamma-2a chain |
| 31 | 802 | 64.8 | 335 | 1 | G2MSAB | Ig gamma-2a chain |
| 32 | 794 | 64.1 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 33 | 785.5 | 63.4 | 322 | 2 | PS0019 | Ig gamma-2a chain |
| 34 | 779 | 62.9 | 474 | 1 | G2MS11 | Ig gamma-2b chain |
| 35 | 774 | 62.5 | 405 | 1 | G2MSBM | Ig gamma-2b chain |
| 36 | 764 | 61.7 | 327 | 2 | S06611 | Ig gamma-2 chain C |
| 37 | 757 | 61.1 | 475 | 2 | S01321 | Ig gamma-2b chain |
| 38 | 707 | 57.1 | 180 | 2 | I46732 | Ig gamma heavy cha |
| 39 | 577.5 | 46.6 | 249 | 2 | S69340 | Ig heavy chain VHI |
| 40 | 574.5 | 46.4 | 218 | 2 | A36040 | Ig heavy chain V-I |
| 41 | 571 | 46.1 | 152 | 2 | S14236 | Ig gamma-1 chain C |
| 42 | 395.5 | 31.9 | 572 | 2 | B46529 | Ig y heavy chain (|
| 43 | 358 | 28.9 | 343 | 2 | S25644 | Ig mu chain C regi |
| 44 | 358 | 28.9 | 453 | 2 | S37768 | Ig mu chain C regi |
| 45 | 357.5 | 28.9 | 549 | 2 | S04845 | Ig heavy chain pre |

ALIGNMENTS

RESULT 1

S31866

Ig gamma-1 chain C region - synthetic

C;Species: synthetic

A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C;Accession: S31866

R;Filpula, D.

submitted to the EMBL Data Library, February 1993

A;Description: Screening method for protein-protein interactions of cloned gene products.

A;Reference number: S31866

A;Accession: S31866

A;Molecule type: mRNA

A;Residues: 1-255 <PIL>

A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID

C;Keywords: immunoglobulin

F;1-22/Region: Escherichia coli outer membrane protein A precursor

F;23-255/Region: human Ig gamma-1 chain C region

Query Match 99.6%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.7e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 2 | DKTHTCPPCPAPELGPGSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD | 61 |
| Db | 29 | DKTHTCPPCPAPELGPGSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD | 88 |
| Qy | 62 | GVEVHNAKTPRREQNSTYRVVSVLTVLDHODWLNKGKCKYKCKVSNKALPAPIETISKAK | 121 |
| Db | 89 | GVEVHNAKTPRREQNSTYRVVSVLTVLDHODWLNKGKCKYKCKVSNKALPAPIETISKAK | 148 |
| Qy | 122 | GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD | 181 |
| Db | 149 | GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD | 208 |
| Qy | 182 | DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK | 228 |
| Db | 209 | DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNHYTQKSLSLSPGK | 255 |

RESULT 2

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004

C;Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034COE; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S3304
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: UNIPARC:UPI00001306FB; EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: Implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Cross-references: UNIPARC:UPI000017378D
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Cross-references: UNIPARC:UPI000017378E
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primärstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: IGHG1

A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 99.6%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.9e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 104 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163
QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 164 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 223
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVVLDS 181
DB 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVVLDS 283
QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 228
DB 284 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 330
RESULT 3
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 99.1%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 2.7e-88;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 148 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 207
QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 208 GVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 267

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Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 268 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 327
Qy 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
Db 328 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 374

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
Mol. Immunol. 28, 319-322, 1991
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 95.3%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 7e-85;
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DKHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
Db 15 DTTHTCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 74
Qy 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 75 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 194
Qy 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKS 221
Db 195 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKS 234

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cd
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 1146; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 5.7e-82;
```

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Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DKHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
Db 151 DTPPCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYVD 210
Qy 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 330
Qy 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 377

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 8.2e-82;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DKHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 61
Db 151 DTPPCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKWYVD 210
Qy 62 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 211 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181
Db 271 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 330
Qy 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
Db 331 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 377

RESULT 7
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32;
```


G3HUWI

Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <PRA>
A:Cross-references: UNIPARC:UPI0000173797
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A:Note: the sequence of residues 42-76 was taken from the reference that follows
R:Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:Cross-references: UNIPARC:UPI0000173798
A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EE', 128-226, 228-289 <WOL>
A:Cross-references: UNIPARC:UPI0000173799
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R:Alexander, A.; Steinmetz, M.; Barriault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: Gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70, 72-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A:Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;
A:Note: a carboxyl-terminal Lys is removed posttranslationally
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMW>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.5%; Score 1121; DB 1; Length 289;
Best Local Similarity 90.3%; Pred. No. 3.6e-80;
Matches 204; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DKHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNQYVD 61

Db 64 DTPPCRCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKYVD 123

Qy 62 GVEVHNAKTKPRBQYNSTRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIETISKAK 121

Db 124 GVQVHNAKTKPRBQYNSTRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIETISKTK 183

Qy 122 GQPRPQVVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 191
Db 184 GQPRPQVVTLPSPREMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 243
Qy 182 DGSFFLYSKLTVDKSRWQOQNFCSCVMHEALHNHVTQKSLSPG 227
Db 244 DGSFFLYSKLTVDKSRWQOQNFCSCVMHEALHNHVTQKSLSPG 289

RESULT 10

GHRB

Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplot;
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BER>
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A:Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'E', 49-71, 'PV', 72-128 <PRA>
A:Cross-references: UNIPARC:UPI00001737AB
R:Wartens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: UNIPARC:UPI000016C5BD; GB:M16426; NID:g165111; PIDN:AAA31289.1; PID:
A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker;
R:Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', 145-161 <FRU>
A:Cross-references: UNIPARC:UPI00001737AC
R:Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: protein
A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', ';
A:Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
C:Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.2%; Score 918.5; DB 1; Length 323;
Best Local Similarity 71.7%; Pred. No. 2.6e-64;
Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MDKTK---HTC--PPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55

Db 91 VDKTVAPFSCSKPTCPPELGGPSVFIIPPCKPKDTLMISRTPEVTCVVVDVSHEDPEVQ 150

A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. An
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
A;Cross-references: UNIPARC:UPI000017379F
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. An
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Cross-references: UNIPARC:UPI00001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI00001737A3
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;21-81/Domain: immunoglobulin homology <IM1>
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

Query Match 71.8%; Score 889; DB 1; Length 329;
Best Local Similarity 72.3%; Pred. No. 5.3e-62;
Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

Qy 6 TCCPCAPPELLGGPSVFLFPPKPTLMIISRTPEVTCVVVDVSHEDPEVKFNYYVDGVEV 65
Db 106 TCPKCPPENLGGPSVFIFFPKPTLMIISLTPRTVCVVVDVSDQDEPEVQFTWFVNDKPV 165
Qy 66 HNAKTKPREQYNTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKQPR 125
Db 166 GNAETKPRVEQYNTTFVESVLPQHODWLRGKEFKCKVYNKALPAPIETKISKAKPR 225
Qy 126 EPQVYVTLPPSRDELTKNOVSLTCLVKGFGYPSDITAVESNGQP--ENNYKTTTPVLDSDG 193
Db 226 MPQVYVTLPPSRDELUSKSGVTCILINIFFPADIHVEASNRVPVSEKYEKNTTPIEDAG 285
Qy 184 SFFLYSLKTVDKSRWQOQNVFSCVSMHEALHNHYTKLSLSLSPG 227

[illegible]

Search completed: April 3, 2006, 05:27:25
Job time : 39 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 05:26:41 ; Search time 457 Seconds
(without alignments)
351.992 Million cell updates/sec

Title: US-10-645-761-2
Perfect score: 1238
Sequence: 1 MDKTHCPCPCAPPELLGPGS.....MHEALHNHYTKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------------|----------------------|
| 1 | 1233 | 99.6 | 330 | 1 | IGHG1_HUMAN | P01857 homo sapien |
| 2 | 1233 | 99.6 | 465 | 2 | Q6GMX6_HUMAN | Q6gmx6 homo sapien |
| 3 | 1233 | 99.6 | 466 | 2 | Q6IN78_HUMAN | Q6in78 homo sapien |
| 4 | 1233 | 99.6 | 469 | 2 | Q569P4_HUMAN | Q569f4 homo sapien |
| 5 | 1233 | 99.6 | 469 | 2 | Q727P5_HUMAN | Q727p5 homo sapien |
| 6 | 1233 | 99.6 | 470 | 2 | Q7Z5W1_HUMAN | Q7z5w1 homo sapien |
| 7 | 1233 | 99.6 | 470 | 2 | Q6PJH4_HUMAN | Q6pjh4 homo sapien |
| 8 | 1233 | 99.6 | 472 | 2 | Q6N089_HUMAN | Q6n089 homo sapien |
| 9 | 1233 | 99.6 | 475 | 2 | Q5EF55_HUMAN | Q5ef55 homo sapien |
| 10 | 1233 | 99.6 | 475 | 2 | Q6GMW7_HUMAN | Q6gmw7 homo sapien |
| 11 | 1233 | 99.6 | 476 | 2 | Q6GMX1_HUMAN | Q6gmx1 homo sapien |
| 12 | 1233 | 99.6 | 679 | 2 | Q96PQ8_HUMAN | Q96pq8 homo sapien |
| 13 | 1229 | 99.3 | 473 | 2 | Q6P0S5_HUMAN | Q6p0s5 homo sapien |
| 14 | 1229 | 99.3 | 475 | 2 | Q6MZ06_HUMAN | Q6mzq6 homo sapien |
| 15 | 1229 | 99.3 | 480 | 2 | Q6N094_HUMAN | Q6n094 homo sapien |
| 16 | 1229 | 99.3 | 481 | 2 | Q6N097_HUMAN | Q6n097 homo sapien |
| 17 | 1229 | 99.3 | 482 | 2 | Q6PYX1_HUMAN | Q7z351 homo sapien |
| 18 | 1227 | 99.1 | 348 | 2 | Q6PYX1_HUMAN | Q6pyx1 homo sapien |
| 19 | 1227 | 99.1 | 473 | 2 | Q6MZV7_HUMAN | Q6mzv7 homo sapien |
| 20 | 1227 | 99.1 | 478 | 2 | Q6PJH1_HUMAN | Q6pjh1 homo sapien |
| 21 | 1227 | 99.1 | 480 | 2 | Q6PJF1_HUMAN | Q6pjf1 homo sapien |
| 22 | 1226 | 99.0 | 466 | 2 | Q6N096_HUMAN | Q6n096 homo sapien |
| 23 | 1222 | 98.7 | 475 | 2 | Q6N095_HUMAN | Q6n095 homo sapien |
| 24 | 1222 | 98.7 | 544 | 2 | Q6PJ95_HUMAN | Q6pj95 homo sapien |
| 25 | 1216 | 98.2 | 487 | 2 | Q65ZL2_HUMAN | Q65z12 homo sapien |
| 26 | 1172 | 94.7 | 475 | 2 | Q5REI7_HUMAN | Q5rei7 pongo sp. iv/ |
| 27 | 1146 | 92.6 | 354 | 2 | Q86T72_HUMAN | Q86tt2 homo sapien |
| 28 | 1146 | 92.6 | 518 | 2 | Q6N030_HUMAN | Q6n030 homo sapien |
| 29 | 1146 | 92.6 | 519 | 2 | Q5EBM2_HUMAN | Q5ebm2 homo sapien |
| 30 | 1142.5 | 92.3 | 326 | 1 | IGHG1_HUMAN | P01859 homo sapien |
| 31 | 1142.5 | 92.3 | 417 | 2 | Q6N093_HUMAN | Q6n093 homo sapien |

| | | | | | | |
|----|--------|------|-----|---|--------------|---------------------|
| 32 | 1142 | 92.2 | 521 | 2 | Q8N4Y9_HUMAN | Q8n4y9 homo sapien |
| 33 | 1139.5 | 92.0 | 484 | 2 | Q6MZU6_HUMAN | Q6mzu6 homo sapien |
| 34 | 1137.5 | 91.9 | 465 | 2 | Q6P6C4_HUMAN | Q6p6c4 homo sapien |
| 35 | 1135 | 91.7 | 327 | 1 | IGHG4_HUMAN | P01861 homo sapien |
| 36 | 1135 | 91.7 | 473 | 2 | Q8TC63_HUMAN | Q8tc63 homo sapien |
| 37 | 1131 | 91.4 | 509 | 2 | Q8NF17_HUMAN | Q8nf17 homo sapien |
| 38 | 1128.5 | 91.2 | 470 | 2 | Q68CN4_HUMAN | Q68cn4 homo sapien |
| 39 | 1126 | 91.0 | 290 | 1 | IGHG3_HUMAN | P01860 homo sapien |
| 40 | 1126 | 91.0 | 476 | 2 | Q6MZX7_HUMAN | Q6mzx7 homo sapien |
| 41 | 918.5 | 74.2 | 323 | 1 | GC_RABIT | P01870 oryctolagus |
| 42 | 909 | 73.4 | 337 | 2 | Q95M34_HORSE | Q95m34 equus caball |
| 43 | 889 | 71.8 | 329 | 1 | IGHG2_CAVPO | P01862 cavia porce |
| 44 | 845.5 | 68.3 | 329 | 1 | GC3_MOUSE | P22436 mus musculus |
| 45 | 845.5 | 68.3 | 470 | 2 | Q7TWK1_MOUSE | Q7tmk1 mus musculus |

ALIGNMENTS

RESULT 1

| ID | IGHG1_HUMAN | STANDARD; | PRT; | 330 AA. |
|----|--|-----------|------|---------|
| AC | P01857; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | |
| DT | 10-MAY-2005 (Rel. 47, Last annotation update) | | | |
| DE | Ig gamma-1 chain C region. | | | |
| GN | Name=IGHG1; | | | |
| OS | Homo sapiens (Human) | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; | | | |
| OC | Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RX | MEDLINE=82274238; PubMed=6287432; | | | |
| RA | Ellison J.W., Berson B.J., Hood L.E.; | | | |
| RT | "The nucleotide sequence of a human immunoglobulin C gamma gene." | | | |
| RL | Nucleic Acids Res. 10:4071-4079(1982). | | | |
| RN | [2] | | | |
| RP | PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). | | | |
| RX | MEDLINE=71064024; PubMed=5489771; | | | |
| RA | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., | | | |
| RA | Waxdal M.J., Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; | | | |
| RL | Biochemistry 9:3161-3170(1970). | | | |
| RN | [3] | | | |
| RP | PROTEIN SEQUENCE OF 136-329 (EU). | | | |
| RX | MEDLINE=71064025; PubMed=5530842; | | | |
| RA | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., | | | |
| RA | Edelman G.M.; | | | |
| RT | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; | | | |
| RL | Biochemistry 9:3171-3181(1970). | | | |
| RN | [4] | | | |
| RP | PROTEIN SEQUENCE (MYELOMA PROTEIN NIE). | | | |
| RX | MEDLINE=77070269; PubMed=826475; | | | |
| RA | Ponstingl H., Hilschmann N.; | | | |
| RT | "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; | | | |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). | | | |
| RN | [5] | | | |
| RP | PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. | | | |
| RX | MEDLINE=83289131; PubMed=6884994; | | | |
| RA | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; | | | |
| RT | "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; | | | |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). | | | |
| RN | [6] | | | |
| RP | DISULFIDE BONDS. | | | |

RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RL Intrachain disulfide bonds";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Daisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC G1M(3) marker and the G1M (non-1) markers.
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC -----
 DR ENBL; J00228; AAC8527.1; ALT_INIT; Genomic_DNA.
 DR PIR; A93433; GHU.
 DR PDB; 1AJ7; X-ray; H=1-103.
 DR PDB; 1AOK; X-ray; H=1-103.
 DR PDB; 1DSB; X-ray; B/H=1-101.
 DR PDB; 1D51; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-330.
 DR PDB; 1FC1; X-ray; A/B=106-329.
 DR PDB; 1FC2; X-ray; D=106-329.
 DR PDB; 1FCG; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I72; X-ray; B/D=1-103.
 DR PDB; 1I1S; X-ray; A/B=107-330.
 DR PDB; 1IIX; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1QOX; X-ray; A/B=119-330.
 DR PDB; 1TB3; X-ray; A/B=107-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR HGNC; HGNC:5525;IGH1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF07654; C1-set; 3.
 DR PROSITE; PS0835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT REGION 1 98 CH1.

| | | | | |
|----|----------|---------|-----------|--------------------------------|
| FT | REGION | 99 | 110 | Hinge. |
| FT | REGION | 221 | 223 | CH2. |
| FT | REGION | 124 | 330 | CH3. |
| FT | CARBOHYD | 180 | 180 | N-linked (GlcNac. . .). |
| FT | DISULFID | 27 | 83 | |
| FT | DISULFID | 103 | 103 | Interchain (with light chain). |
| FT | DISULFID | 109 | 109 | Interchain (with heavy chain). |
| FT | DISULFID | 112 | 112 | Interchain (with heavy chain). |
| FT | DISULFID | 144 | 204 | |
| FT | DISULFID | 250 | 308 | |
| FT | VARIANT | 97 | 97 | K -> R (in G1M(3) marker). |
| FT | | | | /FTId=VAR_003886. |
| FT | VARIANT | 239 | 239 | D -> E (in G1M(non-1) marker). |
| FT | | | | /FTId=VAR_003887. |
| FT | VARIANT | 241 | 241 | L -> M (in G1M(non-1) marker). |
| FT | | | | /FTId=VAR_003888. |
| FT | NON_TER | 1 | 1 | |
| FT | STRAND | 23 | 24 | |
| FT | STRAND | 26 | 33 | |
| FT | STRAND | 38 | 38 | |
| FT | STRAND | 41 | 41 | |
| FT | TURN | 42 | 45 | |
| FT | TURN | 48 | 49 | |
| FT | STRAND | 50 | 52 | |
| FT | STRAND | 57 | 58 | |
| FT | TURN | 59 | 61 | |
| FT | STRAND | 62 | 71 | |
| FT | HELIX | 73 | 75 | |
| FT | TURN | 76 | 78 | |
| FT | STRAND | 82 | 87 | |
| FT | TURN | 88 | 91 | |
| FT | STRAND | 92 | 97 | |
| FT | TURN | 102 | 103 | |
| FT | STRAND | 122 | 126 | |
| FT | HELIX | 130 | 134 | |
| FT | TURN | 136 | 137 | |
| FT | STRAND | 141 | 149 | |
| FT | STRAND | 157 | 162 | |
| FT | TURN | 163 | 164 | |
| FT | STRAND | 165 | 167 | |
| FT | STRAND | 171 | 172 | |
| FT | STRAND | 176 | 177 | |
| FT | TURN | 179 | 180 | |
| FT | STRAND | 183 | 190 | |
| FT | HELIX | 193 | 197 | |
| FT | TURN | 198 | 199 | |
| FT | STRAND | 202 | 207 | |
| FT | TURN | 209 | 210 | |
| FT | STRAND | 215 | 219 | |
| FT | STRAND | 227 | 227 | |
| FT | STRAND | 227 | 234 | |
| FT | HELIX | 238 | 242 | |
| FT | STRAND | 245 | 256 | |
| FT | STRAND | 261 | 266 | |
| FT | TURN | 267 | 268 | |
| FT | STRAND | 269 | 270 | |
| FT | STRAND | 274 | 276 | |
| FT | STRAND | 280 | 281 | |
| FT | TURN | 283 | 284 | |
| FT | STRAND | 287 | 296 | |
| FT | HELIX | 297 | 301 | |
| FT | TURN | 302 | 303 | |
| FT | STRAND | 306 | 311 | |
| FT | TURN | 313 | 314 | |
| FT | HELIX | 316 | 318 | |
| FT | STRAND | 319 | 324 | |
| SQ | SEQUENCE | 330 AA; | 36106 MW; | 3770EE106C2FA33D CRC64; |

Query Match 99.6%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5,8e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 104 DKHTCPCPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYD 163
Qy 62 GVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAK 121
Db 164 GVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAK 223
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 283
Qy 182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGK 228
Db 284 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGK 330

RESULT 2
Q6GMX6 HUMAN
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

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Query Match 99.6%; Score 1233; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DKHTCPCPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYD 61
Db 239 DKHTCPCPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYD 298
Qy 62 GVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAK 121
Db 299 GVEVHNAKTPREBQYNSTYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAK 358
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 359 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 418
Qy 182 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGK 228
Db 419 DGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSLSPGK 465

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RESULT 3

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Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.

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DR SMART: SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
 Query Match 99.6%; Score 1233; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 9.1e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DKHTTCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 DB 243 DKHTTCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 302
 QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
 DB 303 GVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 362
 QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
 DB 363 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 422
 QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228
 DB 423 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 469
 RESULT 6
 Q725W1 HUMAN
 ID Q725W1_HUMAN PRELIMINARY; PRT; 470 AA.
 AC Q725W1;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053984; AAH53984.1; -; mRNA.
 DR HSSP; P01857; 1HZH.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_ci.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483B1A CRC64;
 Query Match 99.6%; Score 1233; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 9.1e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DKHTTCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
 DB 244 DKHTTCCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303
 QY 62 GVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
 DB 304 GVEVHNAKTPREEQNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAK 363
 QY 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
 DB 364 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 423
 QY 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228
 DB 424 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470
 RESULT 7
 Q6PUA4 HUMAN
 ID Q6PUA4_HUMAN PRELIMINARY; PRT; 470 AA.
 AC Q6PUA4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHI protein.
 GN Name=IGHI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH NCI Project;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6PUA4; 20-470.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 9.1e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 244 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303

QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 304 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 363

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
DB 364 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 423

QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
DB 424 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 470

RESULT 8
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CA545781.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

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Query Match 99.6%; Score 1233; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 246 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 305

QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 306 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 365

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
DB 366 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 425

QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 228
DB 426 DGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 472

RESULT 9
Q5BFE5 HUMAN
ID Q5BFE5_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q5BFE5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RT antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AA082028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
FT CHAIN 20 475 Chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400CD7D2859 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 9.3e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61
DB 249 DKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308

QY 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
DB 309 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181

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Db 369 GQPREQVYLLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDLS 428
Qy 182 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
Db 429 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 10
Q6GMW7 HUMAN
ID Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 9.3e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DKHTTCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVSVSHEDPEVKFNKYVD 61
Db 249 DKHTTCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVVSVSHEDPEVKFNKYVD 308
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Qy 62 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 121
Db 309 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 368
Qy 122 GQPREPOVYLLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDLS 181
Db 369 GQPREPOVYLLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDLS 428

RESULT 11
Q6GMX1 HUMAN
ID Q6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDB9D CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 476;
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RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RA Straubeberg R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH65820.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;  
  
Query Match 99.3%; Score 1229; DB 2; Length 473;  
Best Local Similarity 99.6%; Pred. No. 1.9e-91;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 247 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 306  
  
Qy 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 307 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 366  
  
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181  
Db 367 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 426  
  
Qy 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228  
Db 427 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 473  
  
RESULT 14  
Q6MZQ6 HUMAN  
ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6MZQ6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686G11190.  
GN Name=DKFZp686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RA The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CA945972.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Query Match 99.3%; Score 1229; DB 2; Length 480;  
Best Local Similarity 99.6%; Pred. No. 2e-91;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 249 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308  
  
Qy 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 309 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368  
  
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181  
Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 428  
  
Qy 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228  
Db 429 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 475  
  
RESULT 15  
Q6N094 HUMAN  
ID Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6N094;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686O01196.  
GN Name=DKFZp686O01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RA The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Query Match 99.3%; Score 1229; DB 2; Length 480;  
Best Local Similarity 99.6%; Pred. No. 2e-91;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 249 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308  
  
Qy 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 309 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368  
  
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181  
Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 428  
  
Qy 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228  
Db 429 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 475  
  
RESULT 15  
Q6N094 HUMAN  
ID Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6N094;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686O01196.  
GN Name=DKFZp686O01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RA The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;  
  
Query Match 99.3%; Score 1229; DB 2; Length 480;  
Best Local Similarity 99.6%; Pred. No. 2e-91;  
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Db 249 DKHTCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 308  
  
Qy 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121  
Db 309 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 368  
  
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181  
Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 428  
  
Qy 182 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 228  
Db 429 DGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 475
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| Db | 254 | DKHTCPCPAPBELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD | 313 |
| Qy | 62 | GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK | 121 |
| Db | 314 | GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK | 373 |
| Qy | 122 | GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD | 181 |
| Db | 374 | GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD | 433 |
| Qy | 182 | DGSFFLYSKLTVDKSRWQQGNVFCSVMHAEALHNHYTQKSLSLSPGK | 228 |
| Db | 434 | DGSFFLYSKLTVDKSRWQQGNVFCSVMHAEALHNHYTQKSLSLSPGK | 480 |

Search completed: April 3, 2006, 05:34:26
Job time : 457 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 06:16:23 ; Search time 82 Seconds
(without alignments)
1221.687 Million cell updates/sec

Title: US-10-645-761-2

Perfect score: 1238

Sequence: 1 MDXTHTCPPCPAPPELLGPPS.....MHEALHNHYTKSLSLSPGK 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|-------------|
| 1 | 1238 | 100.0 | 228 | 3 AAY96529 | Human IGG |
| 2 | 1238 | 100.0 | 228 | 3 AAB16955 | Human IGG |
| 3 | 1238 | 100.0 | 228 | 4 AAB98953 | Human IGG |
| 4 | 1238 | 100.0 | 228 | 5 ABB04279 | Human IGG |
| 5 | 1238 | 100.0 | 228 | 5 AAU81074 | Human IGG |
| 6 | 1238 | 100.0 | 228 | 5 AAE14310 | Human imm |
| 7 | 1238 | 100.0 | 228 | 5 ABB73410 | Human imm |
| 8 | 1238 | 100.0 | 228 | 5 AAG66012 | Human imm |
| 9 | 1238 | 100.0 | 228 | 5 AAU73018 | Human imm |
| 10 | 1238 | 100.0 | 228 | 6 ABJ38267 | Human IGG |
| 11 | 1238 | 100.0 | 228 | 7 ADN59683 | Human IGG |
| 12 | 1238 | 100.0 | 228 | 8 ADM17708 | Human IGG |
| 13 | 1238 | 100.0 | 228 | 8 ADQ75329 | Human IGG |
| 14 | 1238 | 100.0 | 228 | 3 AAB17957 | FC-MMP in |
| 15 | 1238 | 100.0 | 243 | 5 ABB73425 | FC-MMP in |
| 16 | 1238 | 100.0 | 243 | 7 ADN59746 | Vector 20 |
| 17 | 1238 | 100.0 | 247 | 3 AAB16958 | FC-TMP pr |
| 18 | 1238 | 100.0 | 247 | 5 ABB73411 | FC-TPO mi |
| 19 | 1238 | 100.0 | 248 | 3 AAB17951 | FC-TNF-al |
| 20 | 1238 | 100.0 | 248 | 3 AAB17953 | FC-IL-1 a |
| 21 | 1238 | 100.0 | 248 | 5 ABB73421 | FC-inter1 |
| 22 | 1238 | 100.0 | 248 | 5 ABB73419 | FC-TNF-al |
| 23 | 1238 | 100.0 | 250 | 7 ADD31616 | Ang-2 pep |
| 24 | 1238 | 100.0 | 250 | 8 ADT71978 | Ang-2 pep |

ALIGNMENTS

RESULT 1

AA96529
ID AAY96529 standard; protein; 228 AA.

XX AC AAY96529;

XX DT 04-SEP-2000 (first entry)

XX DE Human IgG1 Fc chain.

XX KW Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;

KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
XX OS Homo sapiens.
XX PN WO200024770-A2.
XX PD 04-MAY-2000.
XX PF 22-OCT-1999; 99WO-US024834.
XX PR 23-OCT-1998; 98US-0105348P.
XX PA (AMGB-) AMGEN INC.
XX PI Liu C, Feige U, Cheestham J;
XX WPI; 2000-365108/31.
XX N-PSDB; AAA29220.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thrombocytopenia.

Disclosure; Page 76-77; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP 1-(L1) nTMP 2], is new. TMP 1 and TMP 2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X₂-X₁¹₀, X₂-X₁¹₁, X₂-X₁¹₂, X₂-X₁¹₃, and X₂-X₁¹₄, X₁¹-X₁¹₀, X₁¹-X₁¹₁, X₁¹-X₁¹₂, X₁¹-X₁¹₃, and X₁¹-X₁¹₄, X₁¹=I, A, V, L, S or R; X₂²=E, D, K or V; X₃³=G or A; X₄⁴=P; X₅⁵=T or S; X₆⁶=L, I, V, A or F; X₇⁷=R or K; X₈⁸=Q, N, or E; X₉⁹=W, Y or F; X₁₀¹⁰=L, I, V, A, F, M, or K; X₁₁¹¹=A, I, V, L, F, S, T, K, H, or E; X₁₂¹²=A, I, V, L, F, G, S, or Q; X₁₃¹³=R, K, T, V, N, Q or G; X₁₄¹⁴=A, I, V, L, F, T, R, E, or G; L₁¹=linker comprising

CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
 CC the c-Mpl receptor which mediates the activity of endogenous
 CC thrombopoietin. The TmPs are useful for increasing the production of
 CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
 CC is useful for treatment of diseases which involve thrombocytopenia, e.g.
 CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
 CC virus associated ITP, and systemic lupus erythematosus
 XX
 SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 3; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
 Db 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy 61 DGEVHNKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIETKTSKA 120
 Db 61 DGEVHNKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIETKTSKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 180
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 2
 AAB16955
 ID AAB16955 standard; protein; 228 AA.
 XX
 AC AAB16955;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human IgG1 Fc protein sequence SEQ ID NO:2.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Homo sapiens.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 PR 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheatham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 DR N-PSDB; AAA69443.
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 FS Claim 7; Page 176-177; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an

CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 3; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
 Db 1 MDKTHTCPPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60

Qy 61 DGEVHNKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIETKTSKA 120
 Db 61 DGEVHNKTKPREEQYNSTYRVVSVLTVTLHODWLNKGEYKCKVSNKALPAPIETKTSKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 180
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
 Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 3
 AAB98953
 ID AAB98953 standard; protein; 228 AA.
 XX
 AC AAB98953;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Human IgG1 Fc region.
 XX
 KW Human, IgG1; immunoglobulin; Fc region; Fc fusion protein; misfolding;
 KW therapy; cancer; osteoarthritis; AIDS; obesity; inflammation;
 KW transplant rejection.
 XX
 OS Homo sapiens.
 XX
 PN WO200134638-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 10-NOV-2000; 2000WO-US030798.
 XX
 PR 12-NOV-1999; 99US-0165188P.
 PR 09-NOV-2000; 2000US-00709704.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Treuheit MJ, O'connor SR, Kosky AA;
 XX
 DR WPI; 2001-335908/35.
 DR N-PSDB; AAH25762.
 XX

PT Correcting disulfide bond misfolds in Fc-containing proteins,
PT particularly therapeutic Fc-containing fusion proteins or antibodies, by
PT treatment with copper halide.

XX PS Claim 30; Fig 5; 59pp; English.

XX CC The present invention describes a process for preparing a
CC pharmacologically active compound, involving preparing a compound
CC comprising an immunoglobulin Fc domain fused to a protein of interest,
CC treating the compound with a copper(II) halide and isolating the treated
CC molecule. This can be used to correct misfolding of Fc domain containing
CC proteins, for use in therapeutic agents which may be used in the
CC treatment of cancer, inflammation, transplant rejection, AIDS,
CC osteoarthritis and obesity. The present sequence is the IgG1 Fc domain

XX SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 4; Length 228;

Best Local Similarity 100.0%; Pred. No. 4.6e-90;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Db 1 MDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGEVHNNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKA 120

Db 61 DGEVHNNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 4

ABB04279

ID ABB04279 standard; protein; 228 AA.

XX AC ABB04279;

XX DT 13-FEB-2002 (first entry)

XX DE Human IgG1 Fc domain.

XX KW Glucagon antagonist; antidiabetic; anti-hormonal; Fc domain;

XX KW non-insulin dependent diabetes mellitus; human; immunoglobulin G; IgG.

XX OS Homo sapiens.

XX PN WO200183527-A2.

XX PD 08-NOV-2001.

XX PF 03-MAY-2001; 2001WO-US014321.

XX PR 03-MAY-2000; 2000US-0201436P.

XX PR 02-MAY-2001; 2001US-00847249.

XX PA (AMGE-) AMGEN INC.

XX PI Marshall WS, Stark KL;

XX XX WPI; 2002-017738/02.

XX DR N-PSDB; ABA03672.

XX PT Compositions comprising glucagon antagonist domains, useful for treating
PT diabetes mellitus.

XX PS Claim 8; Fig 2; 54pp; English.

XX

CC The invention relates to compositions comprising a glucagon antagonist
CC domain and a vehicle, such as a polymer (e.g. PEG or dextran) or,
CC preferably, an Fc domain. The vehicle is covalently attached to the
CC glucagon antagonist domain. The compositions are administered to treat
CC non-insulin dependent diabetes mellitus. The present sequence is the
CC human IgG Fc domain, which may be used as the vehicle in the compositions
CC of the invention

XX SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;

Best Local Similarity 100.0%; Pred. No. 4.6e-90;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Db 1 MDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGEVHNNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKA 120

Db 61 DGEVHNNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 5

AAU81074

ID AAU81074 standard; protein; 228 AA.

XX AC AAU81074;

XX DT 09-APR-2002 (first entry)

XX DE Human IgG1 Fc.

XX KW Human; IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;

XX KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;

XX KW echistatin; integrin; selectin; vinculin; platelet aggregation;

XX KW angiogenesis; tumour; inflammation; autoimmune disease;

XX KW rheumatoid arthritis; osteoporosis.

XX OS Homo sapiens.

XX PN WO200181377-A2.

XX PD 01-NOV-2001.

XX PF 23-APR-2001; 2001WO-US013069.

XX PR 21-APR-2000; 2000US-0198919P.

XX PR 03-MAY-2000; 2000US-0201394P.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Kohno T, Lacey DL, Boone TC;

XX XX WPI; 2002-062025/08.

XX DR N-PSDB; ABK24097.

XX PT Composition comprising integrin or adhesion antagonistic peptide and
PT vehicle, useful for treating or preventing platelet aggregation, has a
PT longer half-life than free peptide.

XX PS Claim 9; Fig 3; 68pp; English.

XX CC The invention relates to a composition comprising an integrin/adhesion

antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (X¹) a-F¹-L¹-(X²)₂ b where; F¹ = Fc domain; X¹ and X² = -(L¹)₁-C-P¹-L¹-(L²)₂-P², (L¹)₁-C-P¹-L¹-(L²)₂-P²-L³-(L⁴)₄-P⁴-L⁴ = same or P³ or (L¹)₁-C-P¹-L¹-(L²)₂-P²-L³-(L⁴)₄-P⁴-L⁴ = same or different (I); L¹-L⁴ = same or different linkers; a-f = 0 or 1, provided at least one of a and b = 1, a nucleic acid that encodes (Ia), an expression vector containing the nucleic acid, host cells containing the vector, producing a pharmaceutically active compound (B) by covalently linking at least one Fc domain to at least one amino acid sequence of a selected randomized (I) and any of six laminin-related peptides (Ib). The compositions are used prophylactically and therapeutically in the same way as (I), e.g. to inhibit platelet aggregation or angiogenesis (tumours), or to treat inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many different forms of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc domain) to (I) increases the half-life (free (I) are normally degraded very quickly in vivo). The present sequence is human IgG1 Fc which is used as a vehicle for the antagonists of the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 228

RESULT 6

AAE14310
ID AAE14310 standard; protein; 228 AA.

XX AAE14310;
XX 07-MAR-2002 (first entry)
XX Human immunoglobulin G (IgG1) Fc.
XX Human; calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
XX immunoglobulin G; IgG; osteopathic.
XX Homo sapiens.
XX WO200183526-A2.
XX 08-NOV-2001.
XX 03-MAY-2001; 2001WO-US014320.
XX 03-MAY-2000; 2000US-0201511P.
XX 02-MAY-2001; 2001US-00847712.
XX (AMGE-) AMGEN INC.
XX Liu C, Marshall WS, Reynolds A;
XX WPI; 2002-034503/04.

DR N-PSDB; AAD23840.
XX Compositions comprising Calcitonin receptor modulator domains, useful for treating osteoporosis.
XX Claim 8; Fig 3; 64pp; English.

XX The invention relates to therapeutic agents that modulate the activity of calcitonin (CT) receptor. Modulators of CT receptor comprise a CT receptor modulating domain and a vehicle such as a polymer or an Fc domain, where the vehicle is covalently attached to the CT receptor modulating domain. The compositions comprising CT receptor modulating domains are used to treat osteoporosis. The present sequence is human immunoglobulin G (IgG1) Fc protein used in the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 228

RESULT 7

ABB73410
ID ABB73410 standard; protein; 228 AA.

XX ABB73410;
XX 05-APR-2002 (first entry)
XX Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; BPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
XX TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
XX MMP inhibitor; antiinflammatory; anticancer; immunosuppressive;
XX cytotoxic; antineoplastic; antithrombotic; antidiabetic; ophthalmological;
XX antianemic; anorectic; antifertility; haemostatic; dermatological;
XX neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
XX cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
XX sleep disorder; neurological degenerative disease; anaemia;
XX thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
XX Fanconi's syndrome.
XX Homo sapiens.
XX WO200183525-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014310.
XX 03-MAY-2000; 2000US-00563286.
XX (AMGE-) AMGEN INC.

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
DR N-PSDB; ABL35760.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Claim 7; Fig 4; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have anti-inflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKLSLSPGK 228

RESULT 8
AAG66012
ID AAG66012 standard; protein; 228 AA.
XX
XX AAG66012;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human immunoglobulin (Ig) G1 Fc region sequence.
XX
XX Apo-AI; amphipathic; pharmaceutical; peptide mimic; antilipemic;
XX anti-HIV; virucide; immunoglobulin; IgG1.
XX
XX Homo sapiens.
OS
XX WO200181376-A2.
PN

XX 01-NOV-2001.
XX 23-APR-2001; 2001WO-US013068.
XX
XX 21-APR-2000; 2000US-0198920P.
PR (AMGE-) AMGEN INC.
XX
XX Kohn T;
FI
XX WPI; 2002-049262/06.
DR N-PSDB; AAI67658.
XX
XX Recombinant or modified therapeutic agents having Apo-AI amphipathic
PT helix peptide activity useful in treatment of hypercholesterolemia and
PT viral infections such as herpes simplex virus, human immunodeficiency
PT virus.
XX
XX Claim 8; Fig 3A-B; 49pp; English.
PS
XX The invention provides a composition comprising a therapeutic agent that
CC has activity similar to Apo-AI amphipathic helix peptide, but with better
CC pharmaceutical characteristics attached to a vehicle through the
CC peptide's N-terminus or C-terminus having a specified formula. The
CC peptide mimic has greater half-life compared to conventional Apo-AI
CC peptide mimic helix peptide. The compositions are useful for treating
CC hypercholesterolemia and viral infection such as HIV, HSV. The present
CC sequence represents the human immunoglobulin (Ig) G1 Fc region which acts
CC as a vehicle
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNNHYTKLSLSPGK 228

RESULT 9
AAU73018
ID AAU73018 standard; protein; 228 AA.
XX
XX AAU73018;
AC
XX 12-MAR-2002 (first entry)
DT
XX Human immunoglobulin G (IgG) Fc region.
DE
XX Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
XX PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;
XX calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
XX osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
XX breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
XX Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
XX Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
XX rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
XX immunoglobulin G; IgG.
KW

```
XX OS Homo sapiens.
XX AC
XX FN WO200181415-A2.
XX PD 01-NOV-2001.
XX PF 27-APR-2001; 2001WO-US013528.
XX PR 27-APR-2000; 2000US-0200053P.
XX PR 28-JUN-2000; 2000US-0214860P.
XX PR 06-FEB-2001; 2001US-0286673P.
XX PR 26-APR-2001; 2001US-00843221.
XX PA (AMGE-) AMGEN INC.
XX PI Kostenuik P, Liu C, Lacey DL;
XX WI; 2002-066435/09.
XX DR N-PSDB; AAS97392.
XX PT Composition, useful for treating osteopenia, comprises parathyroid
XX hormone and parathyroid hormone-related protein receptor modulators.
XX PS Claim 6; Fig 3; 107pp; English.
XX CC The invention relates to a composition (I) comprising modulators of
XX parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
XX which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
XX comprising PTH agonist optionally with a bone resorption inhibitor, such
XX as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
XX oestrogens, oestrogen receptor modulators and tibolone is useful for
XX treating osteopenia. (I) is useful for therapeutic and prophylactic
XX purposes. Antagonists of PTH receptor are useful in treating primary and
XX secondary hyperthyroidism, hypercalcaemia, tumour metastases,
XX particularly breast and prostate cancer, cachexia and anorexia,
XX osteopenia, including various forms of osteoporosis, Paget's disease of
XX bone, osteomyelitis, osteonecrosis or bone cell death, associated with
XX traumatic injury or nontraumatic necrosis associated with Gaucher's
XX disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
XX arthritis, periodontal disease and alopecia. PTH receptor agonists are
XX useful as therapeutic agents in conditions including fracture repair
XX (including healing of non-union fractures), osteopenia, including various
XX forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
XX and parathyroid hormone related protein (PTH/PTHrP) modulators and
XX related amino acid sequences of the invention
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 1238; DB 5; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Qy 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA 120
Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Qy 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYTQKSLSLSPGK 228
RESULT 10
ABJ38267
ID ABJ38267 standard; protein; 228 AA.
```

```
XX ABJ38267;
XX 12-JUN-2003 (first entry)
XX DE Human IgG1 Fc protein SEQ ID No 2.
XX KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
XX systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
XX inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
XX Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
XX glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
XX multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
XX gene therapy; human IgG1Fc; human.
XX OS Homo sapiens.
XX PN WO200292620-A2.
XX PD 21-NOV-2002.
XX PF 13-MAY-2002; 2002WO-US015273.
XX PR 11-MAY-2001; 2001US-0290196P.
XX PA (AMGE-) AMGEN INC.
XX PI Min H, Hsu H;
XX WI; 2003-156719/15.
XX DR N-PSDB; ABT33856.
XX PT New TALL-1-binding polypeptide, useful for modulating the activity of
XX TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
XX autoimmune diseases, cancers or lymphomas.
XX PS Claim 36; Fig 3; 236pp; English.
XX CC The invention relates to a novel TALL-1-binding polypeptide comprising a
XX defined sequence in the specification. The composition is useful in
XX modulating the activity of TALL-1, and in treating, preventing,
XX ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
XX disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
XX lymphoma. The composition may also be used in treating inflammations
XX (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
XX asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
XX glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
XX myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
XX and vasculitis. Disorders may be treated with the novel composition using
XX gene therapy. This sequence represents a human IgG1Fc protein relating to
XX the TALL-1 sequence of the invention
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 1238; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 4.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Qy 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTISKA 120
Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Qy 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYTQKSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYTQKSLSLSPGK 228
```

RESULT 11
 ADN59683
 ID ADN59683 standard; protein; 228 AA.
 AC AC
 AC ADN59683;
 DT 01-JUL-2004 (first entry)
 XX
 XX Human IgG1 Fc amino acid sequence, seq id 32.
 XX
 XX Haemostatic; antianaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 KW lupoid thrombocytopenia; IgG1.
 XX
 OS Homo sapiens.
 XX
 XX WO2003031589-A2.
 XX
 XX 17-APR-2003.
 XX
 XX 11-OCT-2002; 2002WO-US032552.
 XX
 XX 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Min H, Sitney KC, Hartley C;
 XX
 XX WPI; 2003-403101/38.
 DR N-PSDB; ADN59682.
 XX
 XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 XX Disclosure; SEQ ID NO 32; 126pp; English.
 PS
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopenic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents the human IgG1 Fc protein that may be used as a preferred
 CC vehicle of the invention.
 XX
 SQ Sequence 228 AA;
 Query Match 100.0%; Score 1238; DB 7; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDXTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 DB 1 MDXTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 QY 61 DGVEVHNAKTKPREEQVNSTYRVVSVLTVLIHQDLNKGKEYKCKVSNKALPAPIEKTLSKA 120
 DB 61 DGVEVHNAKTKPREEQVNSTYRVVSVLTVLIHQDLNKGKEYKCKVSNKALPAPIEKTLSKA 120
 QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 QY 181 SDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 RESULT 12
 ADM17708
 ID ADM17708 standard; protein; 228 AA.
 XX
 AC ADM17708;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 XX Human IgG1 Fc protein SEQ ID NO:60.
 XX
 XX nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
 KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
 KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
 KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
 KW surgical pain; pain; caustic; demyelinating disease;
 KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
 KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
 KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
 KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
 KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
 KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
 KW burn; allergic skin reaction; pruritus; vitiligo;
 KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
 KW human; IgG1 Fc; immunoglobulin G.
 XX
 OS Homo sapiens.
 XX
 XX WO2004026329-A1.
 XX
 XX 01-APR-2004.
 XX
 XX 19-SEP-2003; 2003WO-US029866.
 PF
 PF 19-SEP-2002; 2002US-0412524P.
 PR 18-SEP-2003; 2003US-0066480.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
 PI
 XX WPI; 2004-283150/26.
 DR N-PSDB; ADM17707.
 DR
 XX Novel peptide capable of modulating nerve growth factor activity, useful
 PT for treating disease or disorder e.g., acute pain, dental pain, cancer,
 PT migraine and collagen vascular disease.
 PT
 XX Claim 16; SEQ ID NO 60; 267pp; English.
 PS
 XX The present invention describes a peptide (I) that is capable of
 CC modulating nerve growth factor (NGF) activity. Also described: (1)
 CC modified peptide (II) comprising (I) and a vehicle, where the modified
 CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
 CC (I); (3) modified peptide (III), its multimers or its salt, where the

peptide is capable of modulating NGF activity; (4) polynucleotide (IV) encoding (I), (II) or (III); (5) expression vector (V) comprising (IV); (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and a vehicle, where the composition of matter is capable of modulating NGF activity; and (8) pharmaceutical composition comprising (I), (II) or (III) and a diluent or carrier. (I) has analgesic activity, and can be used as an inhibitor of NGF. (II) is useful for treating or preventing a disease or disorder associated with NGF activity by administering (I) to human or animal. The disease or disorder chosen from neurologic pain, painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain, migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain, dental pain, pain from trauma, surgical pain, pain resulting from amputation or abscesses, causalgia, demyelinating diseases, trigeminal neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes, acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy, general headache, cluster headache, mixed-vascular and non-vascular syndromes, tension headache, general inflammation, arthritis, rheumatic diseases, lupus, osteoarthritis, inflammatory bowel disorders, inflammatory eye disorders, inflammatory or unstable bladder disorders, skin complaints with inflammatory components, sunburn, carditis, dermatitis, myositis, neuritis, collagen vascular diseases, chronic inflammatory conditions, inflammatory pain associated hyperalgesia and allodynia, neuropathic pain and associated hyperalgesia and allodynia, diabetic neuropathy pain, sympathetically maintained pain, deafferentation syndromes, epithelial tissue damage or dysfunction, herpes simplex, post-herpetic neuralgia, disturbances of visceral motility at respiratory, genitourinary, gastrointestinal or vascular regions, wounds, burns, allergic skin reactions, pruritus, vitiligo, general gastrointestinal disorders, colitis, gastric ulcerations, duodenal ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is also useful for modulating pain or promoting analgesia by administering (I) to human or animal. (I) is also useful in the manufacture of medicament for the treatment of disease or disorder. The present sequence is used in the exemplification of the present invention.

XX SQ Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA 120
 Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
 Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 13

ID ADQ75329
 AC ADQ75329 standard; protein; 228 AA.

XX ADQ75329;

XX 07-OCT-2004 (first entry)

DE Human IgG1 Fc protein.

XX parathyroid hormone; parathyroid hormone-related protein; PTH; PTHrP;
 KW osteopathic; osteopenia; IGF Fc; antibody.

OS Homo sapiens.

XX

PN WO2004060386-A1.

XX 22-JUL-2004.

XX 01-NOV-2002; 2002WO-US036419.

XX 01-NOV-2002; 2002WO-US036419.

XX (AMGE-) AMGEN INC.

XX Kostenuik P, Gegg CV, Jarosinski MA, Kinstler OB;

XX WPI; 2004-543796/52.

XX New composition of matter comprising parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) modulating domain and a vehicle, or its multimers, useful for treating osteopenia.

XX Disclosure; Fig 3A-C; 132pp; English.

XX The invention relates to a composition comprising the formula (I): (I) P1 - (L1)a-P1, where P1 = a vehicle and is attached at the C-terminus of P1- (L1)a or through a sidechain at any residue from residue 14 through the C-terminal residue; P1 = a parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) modulating domain; L1 is a linker; and a = 0 or 1.

XX The composition of matter is useful for treating osteopenia. This sequence corresponds to a human IGF Fc used in the invention.

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA 120

Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228

RESULT 14

ID AAB17957
 AC AAB17957 standard; protein; 243 AA.

XX AAB17957;

XX 31-OCT-2000 (first entry)

XX Fc-MMP inhibitor fusion protein sequence SEQ ID NO:1068.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiaesthatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

XX

PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
XX
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
XX WPI; 2000-350702/30.
XX
DR N-PSDB; AAA69507.
XX
XX Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
XX Example 7; Page 585-586; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antitumour, and
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAA6955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 3; Length 243;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALNHYTKQSLSLSPGK 228
Db 181 SDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALNHYTKQSLSLSPGK 228

RESULT 15
AAB73425
ID AAB73425 standard; protein; 243 AA.
XX
AC AAB73425;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067.
XX
DE Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW

KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014310.
XX
XX 03-MAY-2000; 2000US-00563286.
PR (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
PI WPI; 2002-130313/17.
XX N-PSDB; ABL35775.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Example 7; Fig 25A-B; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. AAB72403 to AAB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 5e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
Db 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180

Db 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228
 Db 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228

RESULT 16

ADN59746
 ID ADN59746 standard; protein; 243 AA.

AC ADN59746;

XX 01-JUL-2004 (first entry)

XX Vector 20003182 encoded amino acid sequence, seq id 95.

XX Haemostatic; antianaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TWP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 KW lupoid thrombocytopaenia.

XX Unidentified.

XX WO2003031589-A2.

PN 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-0328666P.

PR 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

XX Min H, Sitney KC, Hartley C;

XX WPI; 2003-403101/38.

DR N-PSDB; ADN59745.

XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopaenia.

XX Disclosure; SEQ ID NO 95; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopaenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopaenia such as aplastic anaemia,
 CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopaenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopenic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of,
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents the amino acid sequence encoded by a vector for use in

CC constructing C-terminal Fc fusion compounds (i.e. peptide attached at its
 CC N-terminus to the C-terminus of the Fc).

XX Sequence 243 AA;

Query Match 100.0%; Score 1238; DB 7; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPBELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKNNYV 60

Db 1 MDKTHTCPCPAPBELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKNNYV 60

QY 61 DGEVHNATKPREQVNSTYRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKA 120

Db 61 DGEVHNATKPREQVNSTYRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKA 120

QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

Db 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228

RESULT 17

AAB16958

ID AAB16958 standard; protein; 247 AA.

XX AAB16958;

XX 31-OCT-2000 (first entry)

XX Fc-TMP protein sequence SEQ ID NO:6.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

XX Homo sapiens.

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheatham J, Boone TC;

XX WPI; 2000-350702/30.

XX N-PSDB; AAA69444.

XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 21; Page 179-180; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)-b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 5.1e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
 QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
 DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
 QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
 DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 18

ABB73411
 ID ABB73411 standard; protein; 247 AA.

XX AC ABB73411;

XX 05-APR-2002 (first entry)

DE Fc-TPO mimetic peptide (Fc-TMP) amino acid SEQ ID NO:6.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX

PI Feige U, Liu C, Cheestham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR N-PSDB; ABL35761.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.

PS Claim 21; Fig 7; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1238; DB 5; Length 247;

Best Local Similarity 100.0%; Pred. No. 5.1e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120

DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120

QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180

DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

DB 181 SDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 19

AAB17951

ID AAB17951 standard; protein; 248 AA.

XX AC AAB17951;

XX 31-OCT-2000 (first entry)

XX Fc-TNF-alpha inhibitor fusion protein sequence SEQ ID NO:1056.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;

```
KW thrombosis; pharmaceutical.
XX Synthetic.
XX WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US025044.
XX 23-OCT-1998; 98US-0105371P.
XX 22-OCT-1999; 99US-00428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX N-PSDB; AAA69501.
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX Example 4; Page 568-569; 608pp; English.
XX
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
XX (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
XX P3, and P4 = are each independently sequences of pharmacologically active
XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX of a and b is 1. The composition can have cytostatic, antiasthmatic,
XX thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX cells from the present invention can be used for producing pharmaceutical
XX compositions. The compositions are useful for treating cancer, asthma,
XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
XX a Fab domain) can provide a longer half-life or incorporate functions
XX such as Fc receptor binding, protein A binding, complement fixation, and
XX possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
XX AAB18003 represent nucleotide and amino acid sequences used in the
XX exemplification of the present invention
XX
XX Sequence 248 AA;
XX
XX Query Match 100.0%; Score 1238; DB 3; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-90;
XX Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MDKTHCTPCPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
XX Db 1 MDKTHCTPCPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
XX
XX 61 DGVEVHNATKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
XX Db 61 DGVEVHNATKPREEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
XX
XX 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
XX Db 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
XX
XX 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
XX Qy 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
XX
XX 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
XX Db 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
XX
XX RESULT 20
XX AAB17953
XX ID AAB17953 standard; protein; 248 AA.
XX
XX AC AAB17953;
XX
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Db 181 SDGSFFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKQSLSPGK 228
|||||
RESULT 21
ABB73421
ID ABB73421 standard; protein; 248 AA.
XX
AC ABB73421;
XX
DT 05-APR-2002 (first entry)
XX
DE FC-interleukin 1 (IL-1) antagonist fusion nucleic acid SEQ ID NO:1059.
XX
KW Modified peptide; mimetic; FC domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cycostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014310.
XX
XX 03-MAY-2000; 2000US-00563286.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
XX WPI; 2002-130313/17.
XX
XX N-PSDB; ABL35771.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
XX diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Example 5; Fig 21A-B; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
XX cycostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
XX antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
XX neuroprotective activities. (I) can be used as a therapeutic or
XX prophylactic agent as well as for screening purposes. (I) is useful for
XX diagnosing diseases characterised by dysfunction of their associated
XX protein of interest, for identifying normal or abnormal proteins of
XX interest, as a part of diagnostic kit to detect the presence of their
XX proteins of interest in a biological sample. Additionally, (I) is useful
XX for treating inflammatory and autoimmune diseases, tumour growth, cancer,
XX rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
XX infertility, and neurological degenerative diseases. (I), comprising EPO-
XX mimetic compounds are useful for treating disorders characterised by low
XX red blood cell levels such as anaemia. The TPO-mimetic comprising
XX compounds are useful for treating conditions that involve an existing
XX megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
XX deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
XX tumour which result in thrombocytopaenia, systemic lupus erythematosus,
XX and Fanconi's syndrome. ABB72403 to ABB73426 and ABL5695 to ABL5777
XX represent amino acid and nucleic acid sequences used in the
XX exemplification of the present invention
```

```
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 1238; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.1e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDMLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDMLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPRSPQVYTLPPSRDELTKNQVSLTCLVKGPYSDIAVEVESNGQPENNYTKTTPVLD 180
DB 121 KGQPRSPQVYTLPPSRDELTKNQVSLTCLVKGPYSDIAVEVESNGQPENNYTKTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKQSLSPGK 228
RESULT 22
ABB73419
ID ABB73419 standard; protein; 248 AA.
XX
AC ABB73419;
XX
DT 05-APR-2002 (first entry)
XX
DE FC-TNF-alpha inhibitor fusion nucleic acid SEQ ID NO:1055.
XX
KW Modified peptide; mimetic; FC domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW antianaemic; anorectic; antiarthritic; antidiabetic; ophthalmological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014310.
XX
XX 03-MAY-2000; 2000US-00563286.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
XX WPI; 2002-130313/17.
XX
XX N-PSDB; ABL35769.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
XX diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Example 4; Fig 19A-B; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
```

CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antinaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (1) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (1) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (1) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (1), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABLJ35695 to ABLJ35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 1238; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.1e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGEVHNNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
DB 61 DGEVHNNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120
QY 121 KGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

RESULT 23
ADD31616
ID ADD31616 standard; protein; 250 AA.

XX AC ADD31616;

XX DT 15-JAN-2004 (first entry)

XX DE Ang-2 peptibody SEQ ID NO:243.

XX
KW angiotensin-2; Ang-2; angiotensin-2 binding peptide;
KW Ang-2 binding peptide; cytostatic; ophthalmological; anorectic;
KW antiarteriosclerotic; antiinflammatory; antiatherosclerotic;
KW gynaecological; antipsoriatic; angiogenesis inhibitor; gene therapy;
KW tumour growth inhibitor; vascular permeability; plasma leakage; cancer;
KW ocular neovascular disease; obesity; haemangioblastoma; haemangioma;
KW arteriosclerosis; inflammatory disease; inflammatory disorder;
KW atherosclerosis; endometriosis; neoplastic disease; bone-related disease;
KW psoriasis.

XX OS Synthetic.
OS Homo sapiens.

XX PN W02003057134-A2.

XX XX 17-JUL-2003.

XX PF 11-OCT-2002; 2002WO-US032657.

XX XX

PR 11-OCT-2001; 2001US-0328624P.
PR 27-SEP-2002; 2002US-0414155P.
PR 10-OCT-2002; 2002US-0026969S.
XX
XX
PA (AMGE-) AMGEN INC.
XX
XX Oliner J, Min H;
XX
XX WPI; 2003-671400/63.
XX
PT Novel polypeptide capable of binding Ang-2 or its salts, useful for
PT treating cancer, obesity, psoriasis, hemangioma, inflammatory disorders,
PT atherosclerosis, endometriosis.
XX
PS Example 6; SEQ ID NO 243; 376pp; English.

XX
CC The present invention describes a polypeptide (1) capable of binding
CC angiotensin-2 (Ang-2) or its salts. Also described: (1) a fusion
CC polypeptide comprising (1) and a vehicle, where the fusion polypeptides
CC are capable of binding to Ang2, or its salts; (2) a dimer or multimer of
CC (1); (3) a polynucleotide encoding (1); (4) an expression vector
CC comprising a polynucleotide of (3); (5) a host cell comprising the vector
CC of (4); and (6) a pharmaceutical composition comprising (1) in admixture
CC with a carrier. (1) has cytostatic, ophthalmological, anorectic,
CC antiarteriosclerotic, antiinflammatory, antiatherosclerotic,
CC gynaecological and antipsoriatic activities, and can be used as an
CC angiogenesis inhibitor, and in gene therapy. The peptides and
CC polynucleotides are useful for inhibiting undesired angiogenesis,
CC treating angiogenesis, modulating angiogenesis, inhibiting tumour growth
CC characterised by undesired angiogenesis, modulating vascular permeability
CC or plasma leakage in a mammal. They are also useful for treating cancer
CC in a mammal which involves administering them and a chemotherapeutic
CC agent, and also for treating ocular neovascular disease, obesity,
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis in a mammal. (1) is useful
CC for the diagnosis of diseases or conditions characterised by expression
CC of Ang2 or its subunits, and also for treatment of diseases. The present
CC sequence represents an Ang-2 peptibody from the present invention.

XX Sequence 250 AA;

Query Match 100.0%; Score 1238; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.2e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGEVHNNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120

DB 61 DGEVHNNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKKA 120

QY 121 KGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

DB 121 KGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180

QY 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

DB 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

RESULT 24

ADT71978

ID ADT71978 standard; protein; 250 AA.

XX AC ADT71978;

XX DT 13-JAN-2005 (first entry)

XX DE Ang-2 negative control peptibody 4883.

KW inflammatory disease; binding; angiotensin-2; Ang-2; tumour; cancer;
KW angiogenesis; anti-inflammatory; cytostatic; ophthalmological;
KW antiproliferative; antirheumatic; antiarthritic; antiasthmatic; gene therapy;
KW retinopathy; psoriasis; rheumatoid arthritis; asthma.
OS Unidentified.
PN WO2004092215-A2.
XX 28-OCT-2004.
XX 08-APR-2004; 2004WO-US010989.
XX 09-APR-2003; 2003US-00410998.
XX (AMGE-) AMGEN INC.
XX Oliner JD, Min H;
XX WPI; 2004-766831/75.
DR Treating diseases associated with aberrant levels of angiotensin-2 (Ang-
XX 2), such as inflammatory disorders, cancer or retinopathies, comprises
PT administering to a patient an amount of a peptide or peptidyl capable of
PT binding Ang-2.
XX Example 6; SEQ ID NO 243; 341pp; English.
XX The invention relates to a novel method for treating an inflammatory
XX disease. The method comprises administering to a patient a therapeutic
XX amount of a peptide or peptidyl capable of binding angiotensin-2 (Ang-
XX 2), and its pharmaceutical salts. The invention further comprises:
XX peptides that bind to Ang-2; nucleic acid molecules encoding the above
XX peptides and specific binding agents; methods of decreasing a tumour or
XX treating a cancer; and a method of inhibiting angiogenesis. The novel
XX compositions have anti-inflammatory, cytostatic, ophthalmological,
XX antiproliferative, antirheumatic, antiarthritic, and antiasthmatic. The
XX compositions may be used in gene therapy. The composition and methods are
XX useful for treating diseases and conditions associated with aberrant
XX levels of Ang-2, such as inflammatory diseases, cancer, and other
XX diseases such as retinopathies, psoriasis, rheumatoid arthritis and
XX asthma. This sequence represents the Ang-2 negative control peptidyl
XX 4883, of the invention.
SQ Sequence 250 AA;
Query Match 100.0%; Score 1238; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.2e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Qy 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120
Db 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120
Qy 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Qy 181 SDGSPFLYSLKLTVDKSRWQQGNVSCSVMHEALNNHYTKQSLSPGK 228
Db 181 SDGSPFLYSLKLTVDKSRWQQGNVSCSVMHEALNNHYTKQSLSPGK 228
RESULT 25
AAB17955
ID AAB17955 standard; protein; 252 AA.
XX AAB17955;
AC AAB17955;
XX

DT 31-OCT-2000 (first entry)
XX Fe-VSGF antagonist fusion protein sequence SEQ ID NO:1064.
DE
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
XX Synthetic.
OS
XX WO2000024782-A2.
PN
XX 04-MAY-2000.
PD
XX 25-OCT-1999; 99WO-US025044.
PF
XX 23-OCT-1998; 98US-0105371P.
PR
XX 22-OCT-1999; 99US-00428082.
PR
XX (AMGE-) AMGEN INC.
PA
XX Feige U, Liu C, Cheatham J, Boone TC;
PI
XX WPI; 2000-350702/30.
XX N-PSDB; AAA69505.
DR
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
PT
XX Example 6; Page 579-580; 608pp; English.
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX independently selected from -(L1)c-F1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
XX (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where F1, P2,
XX P3, and P4 = are each independently sequences of pharmacologically active
XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX of a and b is 1. The composition can have cytostatic, antiasthmatic,
XX thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX cells from the present invention can be used for producing pharmaceutical
XX compositions. The compositions are useful for treating cancer, asthma,
XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
XX a Fab domain) can provide a longer half-life or incorporate functions
XX such as Fc receptor binding, protein A binding, complement fixation, and
XX possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
XX AAB18003 represent nucleotide and amino acid sequences used in the
XX exemplification of the present invention
SQ Sequence 252 AA;
Query Match 100.0%; Score 1238; DB 3; Length 252;
Best Local Similarity 100.0%; Pred. No. 5.2e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Db 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
Qy 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120
Db 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVTLHQDLNKGKEYCKVSNKALPAPIETKTSKA 120
Qy 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Db 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
Qy 181 SDGSPFLYSLKLTVDKSRWQQGNVSCSVMHEALNNHYTKQSLSPGK 228

CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAB69443 to AAB69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 1238; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.3e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPPELLGSPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGSPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNTSYRVSFLVTLHQDLNGKVEYCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNAKTKPREEQNTSYRVSFLVTLHQDLNGKVEYCKVSNKALPAPIEKTISK 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPOK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPOK 228

RESULT 28
ABB73415
ID ABB73415 standard; protein; 253 AA.
AC ABB73415;
XX
XX
DT 05-APR-2002 (first entry)
XX
DE FC-EPO mimetic peptide (Fc-Emp) amino acid SEQ ID NO:16.
XX
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014310.
XX
XX 03-MAY-2000; 2000US-00563286.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
PI
XX

CC Novel vehicle-peptide molecule or its multimers useful for treating
CC inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
CC diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Example 3; Fig 13; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 1238; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.3e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPPELLGSPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGSPSVFLPPPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNTSYRVSFLVTLHQDLNGKVEYCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNAKTKPREEQNTSYRVSFLVTLHQDLNGKVEYCKVSNKALPAPIEKTISK 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPOK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPOK 228

RESULT 29
AEA18572
ID AEA18572 standard; protein; 259 AA.
AC AEA18572;
XX
XX 28-JUL-2005 (first entry)
DT
XX
XX Amino acid sequence of a mL6-17 peptide fused to an Fc domain.
XX immune reaction; immunogenic therapeutic agent; antibody titer; CTLA-4;
KW immunosuppressive; mL6-17; Fc domain.
XX
XX Synthetic.
XX
XX WO2005044188-A2.
XX
XX 19-MAY-2005.
PD

XX 26-OCT-2004; 2004WO-US035415.
XX 27-OCT-2003; 2003US-0515199P.
XX (AMGE-) AMGEN INC.
XX Khare SD, Feige U;
XX WPI; 2005-346954/35.
XX Decreasing immune reactions in a subject treated with a (potentially)
XX immunogenic therapeutic molecule comprises administering CTLA-4 within an
XX effective time interval relative to the administration of the
XX composition.
XX Example 1; SEQ ID NO 6; 42pp; English.
XX The specification describes a method of decreasing the incidence of an
XX immune reaction in a subject who is given a therapeutic composition
XX comprising a (potentially) immunogenic therapeutic molecule, tolerizing a
XX subject to such a molecule, or decreasing the antibody titer in a subject
XX administered such a molecule. The method comprises administering CTLA-4
XX to the subject within an effective time interval relative to the
XX administration of the therapeutic composition. The CTLA-4 may further
XX comprise an immunoglobulin heavy chain constant region. The method of the
XX invention is useful for modulating an immune response to an immunogenic
XX therapeutic agent. The present sequence represents a mL63-9 peptide fused
XX to an Fc domain. mL6-17 binds to nerve growth factor, and the fusion
XX protein is a therapeutic immunogenic molecule, which was used to
XX demonstrate the method of the invention.
XX Sequence 259 AA;
Query Match 100.0%; Score 1238; DB 9; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.4e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISK 120
QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
RESULT 30
ID AAB16959
XX AAB16959 standard; protein; 268 AA.
XX AAB16959;
XX 31-OCT-2000 (first entry)
XX Fc-TWP-TNP protein sequence SEQ ID NO:8.
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX thrombosis; pharmaceutical.

OS Homo sapiens.
OS Synthetic.
PN WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US025044.
XX 23-OCT-1998; 98US-0105371P.
XX 22-OCT-1999; 99US-00428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX N-PSDB; AAA69445.
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX Example 2; Page 182-183; 608pp; English.
XX The present invention describes composition of matter (I) comprising an
XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX (X1)-a-P1-(X2)-b, where: P1 = an Fc domain; X1 and X2 = are each
XX independently selected from -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
XX (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
XX P3, and P4 = are each independently sequences of pharmacologically active
XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX of a and b is 1. The composition can have cytostatic, antiasthmatic,
XX thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX cells from the present invention can be used for producing pharmaceutical
XX compositions. The compositions are useful for treating cancer, asthma,
XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
XX a Fab domain) can provide a longer half-life or incorporate functions
XX such as Fc receptor binding, protein A binding, complement fixation, and
XX possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
XX AAB16903 represent nucleotide and amino acid sequences used in the
XX exemplification of the present invention
XX Sequence 268 AA;
Query Match 100.0%; Score 1238; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNKTKPREEQYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISK 120
QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
RESULT 31
ID ABB73412
XX ABB73412 standard; protein; 268 AA.
XX ABB73412;
XX 05-APR-2002 (first entry)

XX DE FC-TMP-TMP amino acid SEQ ID NO:8.
 XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; anirrhematic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 PN 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US014310.
 XX 03-MAY-2000; 2000US-00563286.
 PR (AMGE-) AMGEN INC.
 PA Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR N-PSDB; ABL35762.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX Example 2; Fig 8; 176pp; English.
 PS The present invention describes a vehicle-peptide molecule (I) or its
 XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytosstatic, antirrhematic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB74403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 1238; DB 5; Length 268;
 Best Local Similarity 100.0%; Pred. NO. 5.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPELLGPGSVFLPPPKDITLMSRTPVTCVVVDVSHEDPEVKFNWYV 60
 DB 1 MDKTHTCPCPAPELLGPGSVFLPPPKDITLMSRTPVTCVVVDVSHEDPEVKFNWYV 60

QY 61 DGVEVHNAKTKPREOYNSTYRVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKA 120
 DB 61 DGVEVHNAKTKPREOYNSTYRVSVLTVLHODWLNKGKCKVSNKALPAPIEKTISKA 120
 QY 121 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSDIAVEVESNGOPENNYKTTTPVLD 180
 DB 121 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSDIAVEVESNGOPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVFCVSNVHEALHNNHYTKQSLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVFCVSNVHEALHNNHYTKQSLSLSPGK 228
 RESULT 32
 AAY96531
 ID AAY96531 standard; protein; 269 AA.
 XX AC AAY96531;
 XX DT 04-SEP-2000 (first entry)
 XX Human IgG1 Fc TMP fusion protein.
 DE Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
 KW megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
 KW anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
 XX OS Homo sapiens.
 XX WO200024770-A2.
 XX 04-MAY-2000.
 XX 22-OCT-1999; 99WO-US024834.
 XX 23-OCT-1998; 98US-0105348P.
 XX (AMGE-) AMGEN INC.
 XX Liu C, Feige U, Cheetham J;
 PI WPI; 2000-365108/31.
 DR N-PSDB; AAA29229.
 XX Thrombopoietic peptides which activate mpl receptors and increase the
 PT production of platelets or platelet precursors, useful for treatment of
 PT diseases which involve thrombocytopaenia.
 XX Example 2A; Page 49-50; 91pp; English.
 PS A compound which binds to an mpl receptor comprising a thrombopoietin
 XX mimetic peptide (TMP) dimer joined by a linker [TMP 1-(u_1)-TMP 2], is
 CC new. TMP 1 and TMP 2 are amino acid sequences varying from at least 10 to
 CC 14 residues in length comprising X 2-X 1 0, X 2-X 1 1, X 2-X 1 2, X 2-
 CC X 1 3, X 2-X 1 4, X 1-X 1 0, X 1-X 1 1, X 1-X 1 2, X 1-X 1 3, and X 1-
 CC X 1 4. X 1 = I, A, V, L, S or R; X 2 = E, D, K or V; X 3 = G or A; X 4 =
 CC P; X 5 = T or S; X 6 = L, I, V, A or F; X 7 = R or K; X 8 = Q, N, or E;
 CC X 9 = W, Y or F; X 1 0 = L, I, V, A, F, M, or K; X 1 1 = A, I, V, L, F,
 CC S, T, K, H, or E; X 1 2 = A, I, V, L, F, G, S, or Q; X 1 3 = R, K, T, V,
 CC N, Q or G; X 1 4 = A, I, V, L, F, T, R, E, or G; L 1 = linker comprising
 CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
 CC the c-Mpl receptor which mediates the activity of endogenous
 CC thrombopoietin. The TMPs are useful for increasing the production of
 CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
 CC is useful for treatment of diseases which involve thrombocytopaenia, e.g.
 CC aplastic anaemia, immune thrombocytopaenia (ITP), human immunodeficiency
 CC virus associated ITP, and systemic lupus erythematosus
 XX SQ Sequence 269 AA;

Query Match 100.0%; Score 1238; DB 3; Length 269;
 Best Local Similarity 100.0%; Pred. No. 5.7e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 33
AAB16967
ID AAB16967 standard; protein; 277 AA.
XX AC AAB16967;
XX 31-OCT-2000 (first entry)
XX FC-EMP-EMP protein sequence SEQ ID NO:22.
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
OS Homo sapiens.
OS Synthetic.
XX WO200024782-A2.
XX 04-MAY-2000.
XX 25-OCT-1999; 99WO-US025044.
XX 23-OCT-1998; 98US-0105371P.
XX 22-OCT-1999; 99US-00428082.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX N-PSDB; AAA69451.
XX Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX Example 3; Page 201-202; 608pp; English.

CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than

CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 277 AA;
Query Match 100.0%; Score 1238; DB 3; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.9e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 228

RESULT 34
AAB73418
ID AAB73418 standard; protein; 277 AA.
XX AC AAB73418;
XX 05-APR-2002 (first entry)
XX FC-EMP-EMP nucleic acid SEQ ID NO:22.
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antinaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX Homo sapiens.
OS Synthetic.
XX WO200183525-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014310.
XX 03-MAY-2000; 2000US-00563286.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
XX N-PSDB; ABL35768.
XX Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
XX diabetic retinopathy, obesity, sleep disorders and infertility.

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XX Claim 12; Fig 16; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 277 AA;
    Query Match      100.0%; Score 1238; DB 5; Length 277;
    Best Local Similarity 100.0%; Pred. No. 5.9e-90;
    Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
    Db 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
    Qy 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTLSKA 120
    Db 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTLSKA 120
    Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
    Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
    Qy 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
    Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
    RESULT 35
    AAU81169
    ID AAU81169 standard; protein; 282 AA.
    XX
    AC AAU81169;
    XX
    DT 29-AUG-2003 (revised)
    DT 09-APR-2002 (first entry)
    XX
    DE Echinatin/IgG Fc fusion protein.
    XX
    KW IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
    KW immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper;
    KW echistatin; integrin; selectin; vinculin; platelet aggregation;
    KW angiogenesis; tumour; inflammation; autoimmune disease;
    KW rheumatoid arthritis; osteoporosis.
    XX
    OS Echin carinatus.
    OS Homo sapiens.
    OS Chimeric.
    XX
    PN WO200181377-A2.
    XX
    PD 01-NOV-2001.
  
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XX 23-APR-2001; 2001WO-US013069.
XX
XX 21-APR-2000; 2000US-0198919P.
PR 03-MAY-2000; 2000US-0201394P.
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Kohno T, Lacey DL, Boone TC;
XX WPI; 2002-062025/08.
XX N-PSDB; ABK24109.
XX
XX Composition comprising integrin or adhesion antagonistic peptide and
XX vehicle, useful for treating or preventing platelet aggregation, has a
XX longer half-life than free peptide.
XX
XX Example 1; Page 45-46; 68pp; English.
XX
XX The invention relates to a composition comprising an integrin/adhesion
XX antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are
XX based on laminin or saw-scaled viper echistatin and target integrin,
XX selectin or vinculin. Also included are compounds of formula (Ia) and
XX their multimers (X1) a-P1-L-(X2)2 b where; P1 = Fc domain; X1 and X2 =
XX -(L1)1-C-P1-L-(L1)1 C-P1-L-(L2)2 d-P2; (L1)1 C-P1-L-(L2)2 e-
XX P3 or (L1)1 C-P1-L-(L2)2 d-P2-L-(L3)3 e-P3-L-(L4)4 f-P4; P1-P4 = same or
XX different (I); L1-L4 = same or different linkers; a-f = 0 or 1,
XX provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
XX an expression vector containing the nucleic acid, host cells containing
XX the vector, producing a pharmaceutically active compound (B) by
XX covalently linking at least one Fc domain to at least one amino acid
XX sequence of a selected randomized (I) and any of six laminin-related
XX peptides (Ib). The compositions are used prophylactically and
XX therapeutically in the same way as (I), e.g. to inhibit platelet
XX aggregation or angiogenesis (tumours), or to treat inflammation and
XX autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
XX of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
XX domain) to (I) increases the half-life (free (I) are normally degraded
XX very quickly in vivo). The present sequence is a human IgG1 Fc-antagonist
XX peptide fusion compound of the invention. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
SQ Sequence 282 AA;
    Query Match      100.0%; Score 1238; DB 5; Length 282;
    Best Local Similarity 100.0%; Pred. No. 6e-90;
    Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
    Db 1 MDKTHTCPPCPAPPELLGGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNWYV 60
    Qy 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTLSKA 120
    Db 61 DGVEVHNAKTKPREEQNTSYRVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTLSKA 120
    Qy 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
    Db 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD 180
    Qy 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
    Db 181 SDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
    RESULT 36
    AAU49075
    ID AAU49075 standard; protein; 374 AA.
    XX
    AC AAU49075;
    XX
    DT 18-NOV-1998 (first entry)
    XX
  
```

DE Recombinant human MetFc-OB variant 2 protein.
XX
KW Recombinant human MetFc-OB variant 2 protein; chimeric; immunoglobulin;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW diabetes.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
PH Location/Qualifiers
FT Protein
FT 2..374
FT /note= "Recombinant human Fc-OB variant 2 protein"
FT Region
FT 229..374
FT /note= "Human OB protein"
XX
XX
XX WO9828427-A1.
XX
XX
XX 02-JUL-1998.
XX
XX 11-DEC-1997; 97WO-US023183.
XX
XX 20-DEC-1996; 96US-00770973.
XX
XX (AMGE-) AMGEN INC.
XX
XX Mann MB, Hecht RI;
XX
XX WPI; 1998-377658/32.
DR N-PSDB; AAV32902.
XX
XX New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT gall stones or stroke.
XX
XX Claim 2; Fig 5A-5C; 107pp; English.
XX
XX The present sequence represents a recombinant human MetFc-OB variant 2
CC fusion protein having a 5 residue deletion of residues 2-6 of the wild-
CC type Fc-OB protein sequence shown in AAW49073. The invention provides Fc-
CC OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC analogue is linked, either directly or indirectly using a linker, to the
CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC are claimed to demonstrate increased stability and clearance rate and
CC decreased degradation as compared to OB protein or a fusion of Fc to the
CC C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC claimed to be useful for treating excess weight in an individual or
CC animal or for treating co-morbidities associated with excess fat such as
CC diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1238; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 8.4e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

AAW83963
ID AAW83963 standard; protein; 374 AA.
XX
AC AAW83963;
XX
DT 05-FEB-1999 (first entry)
XX
DE Recombinant human metFc-OB protein variant.
XX
XX Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW suspension; variant.
XX
XX Homo sapiens.
XX
XX WO9846257-A1.
XX
XX 22-OCT-1998.
XX
XX 16-APR-1998; 98WO-US007828.
XX
XX 17-APR-1997; 97US-00843971.
PR 14-APR-1998; 98US-00059467.
XX
XX (AMGE-) AMGEN INC.
XX
XX Brems DN, French DL, Speed MA;
PI
XX WPI; 1998-594525/50.
DR N-PSDB; AAV69686.
XX
XX Concentrated suspension of fusion of obesity protein with Fc
PT immunoglobulin fragment - stable at physiological pH, used for e.g.
PT reduction of weight and blood lipid levels, and for treatment of type II
PT diabetes.
XX
XX Claim 2; Fig 6A-C; 47pp; English.
XX
XX This represents a recombinant metFc-OB protein variant which consists of
CC an Fc region of human immunoglobulin (Ig) fused to a human OB (Obesity)
CC protein. The invention provides a human OB protein suspension that
CC contains at least 0.5 mg/ml of the human OB protein derivatised by
CC attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC lipid levels, to treat or prevent diabetes type II, and to increase lean
CC mass and insulin sensitivity. They may be used in conjunction with
CC insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC suppressants etc. These suspensions are stable and active at
CC physiological pH and are ready-for-use formulations that do not require
CC freezing or freeze drying. As they are very concentrated, only small
CC volumes are required and they provide a sustained-release effect, with
CC increased potency and reduced frequency of injection
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1238; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 8.4e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
DB 61 DGVEVHNNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 228

RESULT 37

Db 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228
|||||

RESULT 38

AEBS1285
ID AEB51285 standard; protein; 374 AA.

XX AEBS1285;

AC 06-OCT-2005 (first entry)

XX Recombinant human metFc-OB variant protein SEQ ID NO:15.

DE leptin; fusion protein; diabetes; antidiabetic; endocrine disease;
KW gastrointestinal disease; metabolic disorder; hypoglycemic; osteopathic;
KW obesity.

XX Homo sapiens.

XX US2005163799-A1.

XX 28-JUL-2005.

XX 08-FEB-2005; 2005US-00054085.

XX 22-NOV-1995; 95US-00561732.

XX 20-DEC-1996; 96US-00770973.

XX 07-APR-1998; 98US-00056719.

XX 15-JUN-1998; 98US-00094931.

XX 12-MAR-1999; 99US-00267517.

XX 09-MAY-2000; 2000US-00568528.

XX 06-OCT-2003; 2003US-00679999.

XX (AMGE-) AMGEN INC.

XX Mann MB, Hecht RI, Pellemounter MA, Toombs CF;

XX WPI; 2005-521376/53.

XX N-PSDB; AEB51283.

XX New human leptin fusion protein, useful in increasing lean tissue mass,
PT decreasing the dose of insulin required for treating diabetes, regulating
PT bone resorption, controlling serum glucose levels or increasing insulin
PT sensitivity.

PS Claim 1; SEQ ID NO 15; 43pp; English.

XX The invention relates to a novel isolated human leptin fusion protein
CC comprising any of the fully defined sequences having 379 (each of the 2
CC sequences) or 374 (each of the 2 sequences) amino acids (AEB51279,
CC AEB51282, AEB51285 or AEB51288). The protein is administered to a human
CC suffering from diabetes, and has antidiabetic, hypoglycemic, and
CC osteopathic activity. The human leptin fusion protein is useful in
CC increasing lean tissue mass, in decreasing the dose of insulin required
CC for treating diabetes, in regulating bone resorption, in controlling
CC serum glucose levels or in increasing insulin sensitivity. The present
CC sequence represents a recombinant human metFc-OB variant (obesity/leptin)
CC protein.

XX Sequence 374 AA;

Query Match 100.0%; Score 1238; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 8.4e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Db 1 MDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60

Qy 61 DGVEVHNKTKPREQNSTYRVSVLTVLHODWLNGKVKCKVSNKALPAPIEKTISKA 120

Db 61 DGVEVHNKTKPREQNSTYRVSVLTVLHODWLNGKVKCKVSNKALPAPIEKTISKA 120

Qy 121 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGYPSDIAVEWESNGQPNNYKTTTPVLD 180
Db 121 KGQPREPQVYTLPPSRDELTKQVSLTCLVKGYPSDIAVEWESNGQPNNYKTTTPVLD 180

Qy 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228

Db 181 SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 228

RESULT 39

AAB80904

ID AAB80904 standard; protein; 401 AA.

XX AAB80904;

XX 31-MAY-2001 (first entry)

XX Human metFcDeltaC-OPG(22-194) fusion protein.

XX Human; anticancer; Antimetastatic; Osteogenic; lytic bone disease;
KW multiple myeloma; osteosclerotic bone metastasis; OPG; osteoprotegrin;
KW osteoclast formation inhibition; bone resorption inhibition;
KW immunoglobulin.

XX Homo sapiens.

XX WO200117543-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-US022806.

XX 03-SEP-1999; 99US-00389545.

XX (AMGE-) AMGEN INC.

XX Dunstan CR;

XX WPI; 2001-265936/27.

XX Preventing or treating lytic bone diseases, particularly associated with
PT cancer or metastasis, by administering an osteoprotegrin polypeptide.

PS Claim 11; Fig 8; 87pp; English.

XX The present invention relates to a method for the prevention or treatment
CC of lytic bone disease or multiple myeloma. Also the method can be used
CC for preventing metastasis of cancer to bone or osteosclerotic bone
CC metastasis. The method comprises administering an OPG (osteoprotegrin)
CC polypeptide or OPG fusion protein. The present sequence is one such OPG
CC fusion protein. OPG inhibits formation of osteoclasts (and thus bone
CC resorption) by blocking differentiation from monocytes/macrophage
CC precursors. The OPG polypeptide can be used in a method of preventing or
CC treating lytic bone disease, for preventing metastasis of cancer to bone
CC (e.g. breast, prostate, thyroid, cancer of the kidney, lung, oesophageal,
CC rectal, bladder, cervical, ovarian, liver, cancer of the gastrointestinal
CC tract, multiple myeloma or lymphoma) and preventing the osteosclerotic
CC bone metastasis. The OPG fusion polypeptides are used in the prevention
CC or treatment of loss of bone mass, which occurs in conditions including
CC osteoporosis, such as primary osteoporosis, endocrine osteoporosis
CC (hyperparathyroidism, Cushing's syndrome and acromegaly), hereditary and
CC congenital forms of osteoporosis (osteogenesis imperfecta,
CC homocystinuria, Menkes' syndrome and Riley-Day syndrome) and osteoporosis
CC due to immobilisation of extremities; Paget's disease of bone (osteitis
CC deformans) in adults and juveniles; osteomyelitis, or an infectious
CC lesion in bone; hypercalcaemia resulting from solid tumours (breast, lung
CC and kidney) and haematologic malignancies (multiple myeloma, lymphoma and
CC leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with
CC hyperthyroidism and renal function disorders; osteopaenia following
CC surgery, induced by steroid administration, and associated with disorders
CC of the small and large intestine and with chronic hepatic and renal
CC diseases; osteonecrosis, or bone cell death, associated with traumatic

CC injury or nontraumatic necrosis associated with Gaucher's disease, sickle
CC cell anaemia, systemic lupus erythematosus and other conditions; bone
CC loss due to rheumatoid arthritis; periodontal bone loss; osteoarthritis;
CC prosthetic loosening; and osteolytic metastasis. The OPG fusion proteins
CC are also used in the replacement of structurally sound bone with
CC disorganised bone as seen in Paget's disease of bone (osteitis deformans)
CC in adults and juveniles; hyperparathyroidism, in congenital bone
CC disorders such as fibrous dysplasia, and in osteoclastic bone
CC metastases. The OPG fusion proteins can exhibit increased circulating
CC half-lives and slower clearance times, thereby providing a more sustained
CC activity. The OPG fusion protein comprises a fragment of the human OPG
CC protein and the Fc region of immunoglobulin IgGgamma1 (the hinge, CH2 and
CC CH3 regions; see AAB80897-8)
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 1238; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.2e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

RESULT 40

AAY72922
ID AAY72922 standard; protein; 401 AA.

XX AC AAY72922;

XX DT 13-JUN-2001 (first entry)

XX DE Human met-Fc (lacking 1-5 residues)-OPG (22-194 aa) fusion protein.

XX KW Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;
XX KW therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;
XX KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;
XX KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;
XX KW periodontal.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FH Region 1..228

FT FT /note= Met-human IgG1 Fc region lacking 1-5 residues;
FT FT Corresponds to 6-231 residues of human IgG1 Fc region
FT FT 229..401
FT FT /note= "Derived from human osteoprotegerin fragment (22-
FT FT 194 residues)"

XX PN W0200118203-A1.

XX XX 15-MAR-2001.

XX XX 18-AUG-2000; 2000WO-US022797.

XX XX 03-SEP-1999; 99US-00389782.

XX XX (AMGE-) AMGEN INC.

XX XX

PI Dunstan CR, Wooden SK, Mann MB;
XX WPI; 2001-244572/25.
XX Osteoprotegerin-Fc protein fusions useful for treating bone loss caused
PT by e.g. osteoporosis, Paget's disease and osteomyelitis.
XX Claim 7; Fig 8; 119pp; English.
XX The present sequence is a fusion protein comprising human met-Fc region
CC (lacking 1-5 residues) which is fused with a sequence derived from human
CC osteoprotegerin (OPG; 22-194 residues) by a linker. OPG negatively
CC regulates the formation of osteoclasts in vitro and in vivo. It blocks
CC the differentiation of osteoclasts from monocyte or macrophage precursors
CC and the reabsorption of bone. The OPG-Fc fusion protein is administered
CC for the treatment of bone loss resulting from osteoporosis, Paget's
CC disease, osteomyelitis, hypercalcaemia, osteopenia associated with
CC surgery or steroid administration, osteonecrosis, bone loss due to
CC rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or
CC prosthetic loosening
XX
SQ Sequence 401 AA;

Query Match 100.0%; Score 1238; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.2e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
DB 1 MDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 60
QY 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
DB 61 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 120
QY 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 180
QY 181 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

Search completed: April 3, 2006, 06:19:36
Job time : 84 secs